



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Atkinson, John P.
Hourcade, Dennis
Krych, Malgorzata
- (ii) TITLE OF INVENTION: Modified Truncated Complement System
Regulators
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 2800 One Atlantic Center, 1201 West Peachtree
Street
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: US
(F) ZIP: 30309-3450
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/126,505
(B) FILING DATE: 24-SEP-1993
(C) CLASSIFICATION: 530
- C
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/695,514
(B) FILING DATE: 03-MAY-1991
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: WU101CIP
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (404) 873-8794
(B) TELEFAX: (404) 873-8795

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15
 Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30
 Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45
 Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
 1 5 10 15
 Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
 20 25 30
 Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
 35 40 45
 Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
 1 5 10 15
 Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
 20 25 30
 Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
 35 40 45

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Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 1 5 10 15
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 20 25 30
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 35 40 45
 Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Lys Lys Ala Pro Ile Cys Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Asp Pro Leu Pro Glu Cys Arg
 1 5

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Ser Val Gln
1

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Asp Pro Leu Pro Glu Cys Arg Ser Ser Val Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Thr Lys Pro Pro Ile Cys Gln Asn Ala Ala His
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Pro Tyr Ile Thr Gln Asn Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Arg Thr Thr Phe His Leu Gly Arg Lys Cys Ser Thr Ala Val Ser
1 5 10 15
Pro Ala Thr Thr Ser Glu Gly Leu Arg Leu Cys Ala Ala His Pro Arg
20 25 30
Glu Thr Gly Ala Leu Gln Pro Pro His Val Lys
35 40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..5994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAA TGC AAT GCC CCA GAA TGG CTT CCA TTT GCC AGG CCT ACC AAC CTA 48
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15
ACT GAT GAG TTT GAG TTT CCC ATT GGG ACA TAT CTG AAC TAT GAA TGC 96
Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30
CGC CCT GGT TAT TCC GGA AGA CCG TTT TCT ATC ATC TGC CTA AAA AAC 144
Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45
TCA GTC TGG ACT GGT GCT AAG GAC AGG TGC AGA CGT AAA TCA TGT CGT 192
Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

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AAT CCT CCA GAT CCT GTG AAT GGC ATG GTG CAT GTG ATC AAA GGC ATC Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile 65 70 75 80	240
CAG TTC GGA TCC CAA ATT AAA TAT TCT TGT ACT AAA GGA TAC CGA CTC Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu 85 90 95	288
ATT GGT TCC TCG TCT GCC ACA TGC ATC ATC TCA GGT GAT ACT GTC ATT Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile 100 105 110	336
TGG GAT AAT GAA ACA CCT ATT TGT GAC AGA ATT CCT TGT GGG CTA CCC Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro 115 120 125	384
CCC ACC ATC ACC AAT GGA GAT TTC ATT AGC ACC AAC AGA GAG AAT TTT Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe 130 135 140	432
CAC TAT GGA TCA GTG GTG ACC TAC CGC TGC AAT CCT GGA AGC GGA GGG His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly 145 150 155 160	480
AGA AAG GTG TTT GAG CTT GTG GGT GAG CCC TCC ATA TAC TGC ACC AGC Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser 165 170 175	528
AAT GAC GAT CAA GTG GGC ATC TGG AGC GGC CCC GCC CCT CAG TGC ATT Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile 180 185 190	576
ATA CCT AAC AAA TGC ACG CCT CCA AAT GTG GAA AAT GGA ATA TTG GTA Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val 195 200 205	624
TCT GAC AAC AGA AGC TTA TTT TCC TTA AAT GAA GTT GTG GAG TTT AGG Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg 210 215 220	672
TGT CAG CCT GGC TTT GTC ATG AAA GGA CCC CGC CGT GTG AAG TGC CAG Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln 225 230 235 240	720
GCC CTG AAC AAA TGG GAG CCG GAG CTA CCA AGC TGC TCC AGG GTA TGT Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys 245 250 255	768
CAG CCA CCT CCA GAT GTC CTG CAT GCT GAG CGT ACC CAA AGG GAC AAG Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys 260 265 270	816
GAC AAC TTT TCA CCT GGG CAG GAA GTG TTC TAC AGC TGT GAG CCC GGC Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly 275 280 285	864
TAC GAC CTC AGA GGG GCT GCG TCT ATG CGC TGC ACA CCC CAG GGA GAC Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp 290 295 300	912

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TGG	AGC	CCT	GCA	GCC	CCC	ACA	TGT	GAA	GTG	AAA	TCC	TGT	GAT	GAC	TTC	960
Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	Asp	Phe	
305					310					315					320	
ATG	GGC	CAA	CTT	CTT	AAT	GGC	CGT	GTG	CTA	TTT	CCA	GTA	AAT	CTC	CAG	1008
Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	Leu	Gln	
				325					330						335	
CTT	GGA	GCA	AAA	GTG	GAT	TTT	GTT	TGT	GAT	GAA	GGA	TTT	CAA	TTA	AAA	1056
Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	Leu	Lys	
			340						345						350	
GGC	AGC	TCT	GCT	AGT	TAC	TGT	GTC	TTG	GCT	GGA	ATG	GAA	AGC	CTT	TGG	1104
Gly	Ser	Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met		Glu	Ser	Leu	
			355					360					365			
AAT	AGC	AGT	GTT	CCA	GTG	TGT	GAA	CAA	ATC	TTT	TGT	CCA	AGT	CCT	CCA	1152
Asn	Ser	Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser	Pro	Pro	
			370					375					380			
GTT	ATT	CCT	AAT	GGG	AGA	CAC	ACA	GGA	AAA	CCT	CTG	GAA	GTC	TTT	CCC	1200
Val	Ile	Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val	Phe	Pro	
385					390					395					400	
TTT	GGA	AAA	GCA	GTA	AAT	TAC	ACA	TGC	GAC	CCC	CAC	CCA	GAC	AGA	GGG	1248
Phe	Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly	
				405					410						415	
ACG	AGC	TTC	GAC	CTC	ATT	GGA	GAG	AGC	ACC	ATC	CGC	TGC	ACA	AGT	GAC	1296
Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asp	
			420						425						430	
CCT	CAA	GGG	AAT	GGG	GTT	TGG	AGC	AGC	CCT	GCC	CCT	CGC	TGT	GGA	ATT	1344
Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Gly	Ile	
			435					440							445	
CTG	GGT	CAC	TGT	CAA	GCC	CCA	GAT	CAT	TTT	CTG	TTT	GCC	AAG	TTG	AAA	1392
Leu	Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala	Lys	Leu	Lys	
			450					455							460	
ACC	CAA	ACC	AAT	GCA	TCT	GAC	TTT	CCC	ATT	GGG	ACA	TCT	TTA	AAG	TAC	1440
Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	Lys	Tyr	
465					470					475					480	
GAA	TGC	CGT	CCT	GAG	TAC	TAC	GGG	AGG	CCA	TTC	TCT	ATC	ACA	TGT	CTA	1488
Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr	Cys	Leu	
				485					490						495	
GAT	AAC	CTG	GTC	TGG	TCA	AGT	CCC	AAA	GAT	GTC	TGT	AAA	CGT	AAA	TCA	1536
Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys	Arg	Lys	Ser	
				500					505						510	
TGT	AAA	ACT	CCT	CCA	GAT	CCA	GTG	AAT	GGC	ATG	GTG	CAT	GTG	ATC	ACA	1584
Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Thr	
			515					520							525	
GAC	ATC	CAG	GTT	GGA	TCC	AGA	ATC	AAC	TAT	TCT	TGT	ACT	ACA	GGG	CAC	1632
Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile	Asn	Tyr	Ser	Cys	Thr	Thr	Gly	His	
			530					535							540	

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CGA	CTC	ATT	GGT	CAC	TCA	TCT	GCT	GAA	TGT	ATC	CTC	TCG	GGC	AAT	GCT	1680
Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Ala	
545					550					555					560	
GCC	CAT	TGG	AGC	ACG	AAG	CCG	CCA	ATT	TGT	CAA	CGA	ATT	CCT	TGT	GGG	1728
Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly	
				565					570						575	
CTA	CCC	CCC	ACC	ATC	GCC	AAT	GGA	GAT	TTC	ATT	AGC	ACC	AAC	AGA	GAG	1776
Leu	Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	
			580					585						590		
AAT	TTT	CAC	TAT	GGA	TCA	GTG	GTG	ACC	TAC	CGC	TGC	AAT	CCT	GGA	AGC	1824
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	
		595					600						605			
GGA	GGG	AGA	AAG	GTG	TTT	GAG	CTT	GTG	GGT	GAG	CCC	TCC	ATA	TAC	TGC	1872
Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	
	610					615					620					
ACC	AGC	AAT	GAC	GAT	CAA	GTG	GGC	ATC	TGG	AGC	GGC	CCG	GCC	CCT	CAG	1920
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	
625					630					635					640	
TGC	ATT	ATA	CCT	AAC	AAA	TGC	ACG	CCT	CCA	AAT	GTG	GAA	AAT	GGA	ATA	1968
Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	
				645					650					655		
TTG	GTA	TCT	GAC	AAC	AGA	AGC	TTA	TTT	TCC	TTA	AAT	GAA	GTT	GTG	GAG	2016
Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	
			660					665						670		
TTT	AGG	TGT	CAG	CCT	GGC	TTT	GTC	ATG	AAA	GGA	CCC	CGC	CGT	GTG	AAG	2064
Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	
		675					680						685			
TGC	CAG	GCC	CTG	AAC	AAA	TGG	GAG	CCG	GAG	CTA	CCA	AGC	TGC	TCC	AGG	2112
Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	
	690					695					700					
GTA	TGT	CAG	CCA	CCT	CCA	GAT	GTC	CTG	CAT	GCT	GAG	CGT	ACC	CAA	AGG	2160
Val	Cys	Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	
705					710					715					720	
GAC	AAG	GAC	AAC	TTT	TCA	CCC	GGG	CAG	GAA	GTG	TTC	TAC	AGC	TGT	GAG	2208
Asp	Lys	Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	
				725					730						735	
CCC	GGC	TAT	GAC	CTC	AGA	GGG	GCT	GCG	TCT	ATG	CGC	TGC	ACA	CCC	CAG	2256
Pro	Gly	Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	
			740					745						750		
GGA	GAC	TGG	AGC	CCT	GCA	GCC	CCC	ACA	TGT	GAA	GTG	AAA	TCC	TGT	GAT	2304
Gly	Asp	Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	
		755					760						765			
GAC	TTC	ATG	GGC	CAA	CTT	CTT	AAT	GGC	CGT	GTG	CTA	TTT	CCA	GTA	AAT	2352
Asp	Phe	Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	
	770					775					780					

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CTC	CAG	CTT	GGA	GCA	AAA	GTG	GAT	TTT	GTT	TGT	GAT	GAA	GGA	TTT	CAA	2400
Leu	Gln	Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	
785					790					795					800	
TTA	AAA	GGC	AGC	TCT	GCT	AGT	TAT	TGT	GTC	TTG	GCT	GGA	ATG	GAA	AGC	2448
Leu	Lys	Gly	Ser	Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met	Glu	Ser	
				805					810					815		
CTT	TGG	AAT	AGC	AGT	GTT	CCA	GTG	TGT	GAA	CAA	ATC	TTT	TGT	CCA	AGT	2496
Leu	Trp	Asn	Ser	Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser	
			820					825					830			
CCT	CCA	GTT	ATT	CCT	AAT	GGG	AGA	CAC	ACA	GGA	AAA	CCT	CTG	GAA	GTC	2544
Pro	Pro	Val	Ile	Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val	
		835					840					845				
TTT	CCC	TTT	GGA	AAA	GCA	GTA	AAT	TAC	ACA	TGC	GAC	CCC	CAC	CCA	GAC	2592
Phe	Pro	Phe	Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	
850						855					860					
AGA	GGG	ACG	AGC	TTC	GAC	CTC	ATT	GGA	GAG	AGC	ACC	ATC	CGC	TGC	ACA	2640
Arg	Gly	Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	
865					870					875					880	
AGT	GAC	CCT	CAA	GGG	AAT	GGG	GTT	TGG	AGC	AGC	CCT	GCC	CCT	CGC	TGT	2688
Ser	Asp	Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	
				885					890					895		
GGA	ATT	CTG	GGT	CAC	TGT	CAA	GCC	CCA	GAT	CAT	TTT	CTG	TTT	GCC	AAG	2736
Gly	Ile	Leu	Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala	Lys	
			900					905					910			
TTG	AAA	ACC	CAA	ACC	AAT	GCA	TCT	GAC	TTT	CCC	ATT	GGG	ACA	TCT	TTA	2784
Leu	Lys	Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	
		915					920					925				
AAG	TAC	GAA	TGC	CGT	CCT	GAG	TAC	TAC	GGG	AGG	CCA	TTC	TCT	ATC	ACA	2832
Lys	Tyr	Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr	
	930					935					940					
TGT	CTA	GAT	AAC	CTG	GTC	TGG	TCA	AGT	CCC	AAA	GAT	GTC	TGT	AAA	CGT	2880
Cys	Leu	Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys	Arg	
945					950					955					960	
AAA	TCA	TGT	AAA	ACT	CCT	CCA	GAT	CCA	GTG	AAT	GGC	ATG	GTG	CAT	GTG	2928
Lys	Ser	Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	
				965					970					975		
ATC	ACA	GAC	ATC	CAG	GTT	GGA	TCC	AGA	ATC	AAC	TAT	TCT	TGT	ACT	ACA	2976
Ile	Thr	Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile	Asn	Tyr	Ser	Cys	Thr	Thr	
			980					985					990			
GGG	CAC	CGA	CTC	ATT	GGT	CAC	TCA	TCT	GCT	GAA	TGT	ATC	CTC	TCA	GGC	3024
Gly	His	Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	
		995					1000					1005				
AAT	ACT	GCC	CAT	TGG	AGC	ACG	AAG	CCG	CCA	ATT	TGT	CAA	CGA	ATT	CCT	3072
Asn	Thr	Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	
	1010						1015					1020				

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Cont

TGT GGG CTA CCC CCA ACC ATC GCC AAT GGA GAT TTC ATT AGC ACC AAC Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn 1025 1030 1035 1040	3120
AGA GAG AAT TTT CAC TAT GGA TCA GTG GTG ACC TAC CGC TGC AAT CTT Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu 1045 1050 1055	3168
GGA AGC AGA GGG AGA AAG GTG TTT GAG CTT GTG GGT GAG CCC TCC ATA Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile 1060 1065 1070	3216
TAC TGC ACC AGC AAT GAC GAT CAA GTG GGC ATC TGG AGC GGC CCC GCC Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala 1075 1080 1085	3264
CCT CAG TGC ATT ATA CCT AAC AAA TGC ACG CCT CCA AAT GTG GAA AAT Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn 1090 1095 1100	3312
GGA ATA TTG GTA TCT GAC AAC AGA AGC TTA TTT TCC TTA AAT GAA GTT Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val 1105 1110 1115 1120	3360
GTG GAG TTT AGG TGT CAG CCT GGC TTT GTC ATG AAA GGA CCC CGC CGT Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg 1125 1130 1135	3408
GTG AAG TGC CAG GCC CTG AAC AAA TGG GAG CCA GAG TTA CCA AGC TGC Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys 1140 1145 1150	3456
TCC AGG GTG TGT CAG CCG CCT CCA GAA ATC CTG CAT GGT GAG CAT ACC Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr 1155 1160 1165	3504
CCA AGC CAT CAG GAC AAC TTT TCA CCT GGG CAG GAA GTG TTC TAC AGC Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser 1170 1175 1180	3552
TGT GAG CCT GGC TAT GAC CTC AGA GGG GCT GCG TCT CTG CAC TGC ACA Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr 1185 1190 1195 1200	3600
CCC CAG GGA GAC TGG AGC CCT GAA GCC CCG AGA TGT GCA GTG AAA TCC Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser 1205 1210 1215	3648
TGT GAT GAC TTC TTG GGT CAA CTC CCT CAT GGC CGT GTG CTA TTT CCA Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro 1220 1225 1230	3696
CTT AAT CTC CAG CTT GGG GCA AAG GTG TCC TTT GTC TGT GAT GAA GGG Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly 1235 1240 1245	3744
TTT CGC TTA AAG GGC AGT TCC GTT AGT CAT TGT GTC TTG GTT GGA ATG Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met 1250 1255 1260	3792

c!
Cont.

AGA AGC CTT TGG AAT AAC AGT GTT CCT GTG TGT GAA CAT ATC TTT TGT	3840
Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys	
1265 1270 1275 1280	
CCA AAT CCT CCA GCT ATC CTT AAT GGG AGA CAC ACA GGA ACT CCC TCT	3888
Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser	
1285 1290 1295	
GGA GAT ATT CCC TAT GGA AAA GAA ATA TCT TAC ACA TGT GAC CCC CAC	3936
Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His	
1300 1305 1310	
CCA GAC AGA GGG ATG ACC TTC AAC CTC ATT GGG GAG AGC ACC ATC CGC	3984
Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg	
1315 1320 1325	
TGC ACA AGT GAC CCT CAT GGG AAT GGG GTT TGG AGC AGC CCT GCC CCT	4032
Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro	
1330 1335 1340	
CGC TGT GAA CTT TCT GTT CGT GCT GGT CAC TGT AAA ACC CCA GAG CAG	4080
Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln	
1345 1350 1355 1360	
TTT CCA TTT GCC AGT CCT ACG ATC CCA ATT AAT GAC TTT GAG TTT CCA	4128
Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro	
1365 1370 1375	
GTC GGG ACA TCT TTG AAT TAT GAA TGC CGT CCT GGG TAT TTT GGG AAA	4176
Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys	
1380 1385 1390	
ATG TTC TCT ATC TCC TGC CTA GAA AAC TTG GTC TGG TCA AGT GTT GAA	4224
Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu	
1395 1400 1405	
GAC AAC TGT AGA CGA AAA TCA TGT GGA CCT CCA CCA GAA CCC TTC AAT	4272
Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn	
1410 1415 1420	
GGA ATG GTG CAT ATA AAC ACA GAT ACA CAG TTT GGA TCA ACA GTT AAT	4320
Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn	
1425 1430 1435 1440	
TAT TCT TGT AAT GAA GGG TTT CGA CTC ATT GGT TCC CCA TCT ACT ACT	4368
Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr	
1445 1450 1455	
TGT CTC GTC TCA GGC AAT AAT GTC ACA TGG GAT AAG AAG GCA CCT ATT	4416
Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile	
1460 1465 1470	
TGT GAG ATC ATA TCT TGT GAG CCA CCT CCA ACC ATA TCC AAT GGA GAC	4464
Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp	
1475 1480 1485	
TTC TAC AGC AAC AAT AGA ACA TCT TTT CAC AAT GGA ACG GTG GTA ACT	4512
Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr	
1490 1495 1500	

cl
cont.

TAC CAG TGC CAC ACT GGA CCA GAT GGA GAA CAG CTG TTT GAG CTT GTG Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val 1505 1510 1515 1520	4560
GGA GAA CGG TCA ATA TAT TGC ACC AGC AAA GAT GAT CAA GTT GGT GTT Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val 1525 1530 1535	4608
TGG AGC AGC CCT CCC CCT CGG TGT ATT TCT ACT AAT AAA TGC ACA GCT Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala 1540 1545 1550	4656
CCA GAA GTT GAA AAT GCA ATT AGA GTA CCA GGA AAC AGG AGT TTC TTT Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe 1555 1560 1565	4704
TCC CTC ACT GAG ATC ATC AGA TTT AGA TGT CAG CCC GGG TTT GTC ATG Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met 1570 1575 1580	4752
GTA GGG TCC CAC ACT GTG CAG TGC CAG ACC AAT GGC AGA TGG GGG CCC Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro 1585 1590 1595 1600	4800
AAG CTG CCA CAC TGC TCC AGG GTG TGT CAG CCG CCT CCA GAA ATC CTG Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu 1605 1610 1615	4848
CAT GGT GAG CAT ACC CTA AGC CAT CAG GAC AAC TTT TCA CCT GGG CAG His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln 1620 1625 1630	4896
GAA GTG TTC TAC AGC TGT GAG CCC AGC TAT GAC CTC AGA GGG GCT GCG Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala 1635 1640 1645	4944
TCT CTG CAC TGC ACG CCC CAG GGA GAC TGG AGC CCT GAA GCC CCT AGA Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg 1650 1655 1660	4992
TGT ACA GTG AAA TCC TGT GAT GAC TTC CTG GGC CAA CTC CCT CAT GGC Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly 1665 1670 1675 1680	5040
CGT GTG CTA CTT CCA CTT AAT CTC CAG CTT GGG GCA AAG GTG TCC TTT Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe 1685 1690 1695	5088
GTT TGC GAT GAA GGG TTC CGA TTA AAA GGC AGG TCT GCT AGT CAT TGT Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys 1700 1705 1710	5136
GTC TTG GCT GGA ATG AAA GCC CTT TGG AAT AGC AGT GTT CCA GTG TGT Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys 1715 1720 1725	5184
GAA CAA ATC TTT TGT CCA AAT CCT CCA GCT ATC CTT AAT GGG AGA CAC Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His 1730 1735 1740	5232

C1
Cont.

ACA GGA ACT CCC TTT GGA GAT ATT CCC TAT GGA AAA GAA ATA TCT TAC Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr 1745 1750 1755 1760	5280
GCA TGC GAC ACC CAC CCA GAC AGA GGG ATG ACC TTC AAC CTC ATT GGG Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly 1765 1770 1775	5328
GAG AGC TCC ATC CGC TGC ACA AGT GAC CCT CAA GGG AAT GGG GTT TGG Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp 1780 1785 1790	5376
AGC AGC CCT GCC CCT CGC TGT GAA CTT TCT GTT CCT GCT GCC TGC CCA Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro 1795 1800 1805	5424
CAT CCA CCC AAG ATC CAA AAC GGG CAT TAC ATT GGA GGA CAC GTA TCT His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser 1810 1815 1820	5472
CTA TAT CTT CCT GGG ATG ACA ATC AGC TAC ACT TGT GAC CCC GGC TAC Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr 1825 1830 1835 1840	5520
CTG TTA GTG GGA AAG GGC TTC ATT TTC TGT ACA GAC CAG GGA ATC TGG Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp 1845 1850 1855	5568
AGC CAA TTG GAT CAT TAT TGC AAA GAA GTA AAT TGT AGC TTC CCA CTG Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu 1860 1865 1870	5616
TTT ATG AAT GGA ATC TCG AAG GAG TTA GAA ATG AAA AAA GTA TAT CAC Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His 1875 1880 1885	5664
TAT GGA GAT TAT GTG ACT TTG AAG TGT GAA GAT GGG TAT ACT CTG GAA Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu 1890 1895 1900	5712
GGC AGT CCC TGG AGC CAG TGC CAG GCG GAT GAC AGA TGG GAC CCT CCT Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro 1905 1910 1915 1920	5760
CTG GCC AAA TGT ACC TCT CGT GCA CAT GAT GCT CTC ATA GTT GGC ACT Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val Gly Thr 1925 1930 1935	5808
TTA TCT GGT ACG ATC TTC TTT ATT TTA CTC ATC ATT TTC CTC TCT TGG Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu Ser Trp 1940 1945 1950	5856
ATA ATT CTA AAG CAC AGA AAA GGC AAT AAT GCA CAT GAA AAC CCT AAA Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn Pro Lys 1955 1960 1965	5904
GAA GTG GCT ATC CAT TTA CAT TCT CAA GGA GGC AGC AGC GTT CAT CCC Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val His Pro 1970 1975 1980	5952

Cont.

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Gln 1	Cys	Asn	Ala	Pro 5	Glu	Trp	Leu	Pro	Phe 10	Ala	Arg	Pro	Thr	Asn 15	Leu
Thr	Asp	Glu	Phe 20	Glu	Phe	Pro	Ile	Gly 25	Thr	Tyr	Leu	Asn	Tyr 30	Glu	Cys
Arg	Pro	Gly 35	Tyr	Ser	Gly	Arg	Pro 40	Phe	Ser	Ile	Ile	Cys 45	Leu	Lys	Asn
Ser	Val 50	Trp	Thr	Gly	Ala	Lys 55	Asp	Arg	Cys	Arg 60	Arg	Lys	Ser	Cys	Arg
Asn 65	Pro	Pro	Asp	Pro	Val 70	Asn	Gly	Met	Val	His 75	Val	Ile	Lys	Gly	Ile 80
Gln	Phe	Gly	Ser	Gln 85	Ile	Lys	Tyr	Ser	Cys 90	Thr	Lys	Gly	Tyr	Arg 95	Leu

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110
 Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125
 Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140
 His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350
 Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

C
 cont.

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445
 Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460
 Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480
 Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495
 Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510
 Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
 515 520 525
 Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540
 Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560
 Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575
 Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 645 650 655
 Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 660 665 670
 Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 675 680 685
 Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 690 695 700
 Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 705 710 715 720
 Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 725 730 735
 Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750
 Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

C
 Cont.

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780
 Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895
 Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910
 Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925
 Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940
 Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960
 Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005
 Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 1010 1015 1020
 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 1025 1030 1035 1040
 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu
 1045 1050 1055
 Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 1060 1065 1070
 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 1075 1080 1085
 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 1090 1095 1100

C
 Cont.

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 1105 1110 1115 1120
 Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
 1125 1130 1135
 Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 1140 1145 1150
 Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr
 1155 1160 1165
 Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 1170 1175 1180
 Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr
 1185 1190 1195 1200
 Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser
 1205 1210 1215
 Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro
 1220 1225 1230
 Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly
 1235 1240 1245
 Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met
 1250 1255 1260
 Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys
 1265 1270 1275 1280
 Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser
 1285 1290 1295
 Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His
 1300 1305 1310
 Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg
 1315 1320 1325
 Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 1330 1335 1340
 Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln
 1345 1350 1355 1360
 Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro
 1365 1370 1375
 Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys
 1380 1385 1390
 Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu
 1395 1400 1405
 Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn
 1410 1415 1420
 Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn
 1425 1430 1435 1440

C
 Cont.

Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr
 1445 1450 1455
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile
 1460 1465 1470
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp
 1475 1480 1485
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr
 1490 1495 1500
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val
 1505 1510 1515 1520
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val
 1525 1530 1535
 Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
 1540 1545 1550
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe
 1555 1560 1565
 Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met
 1570 1575 1580
 Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro
 1585 1590 1595 1600
 Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu
 1605 1610 1615
 His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln
 1620 1625 1630
 Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala
 1635 1640 1645
 Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg
 1650 1655 1660
 Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly
 1665 1670 1675 1680
 Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe
 1685 1690 1695
 Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys
 1700 1705 1710
 Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys
 1715 1720 1725
 Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His
 1730 1735 1740
 Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr
 1745 1750 1755 1760
 Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly
 1765 1770 1775

cl
 Cont.

Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
 1780 1785 1790
 Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro
 1795 1800 1805
 His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser
 1810 1815 1820
 Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr
 1825 1830 1835 1840
 Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp
 1845 1850 1855
 Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu
 1860 1865 1870
 Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His
 1875 1880 1885
 Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu
 1890 1895 1900
 Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro
 1905 1910 1915 1920
 Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val Gly Thr
 1925 1930 1935
 Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu Ser Trp
 1940 1945 1950
 Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn Pro Lys
 1955 1960 1965
 Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val His Pro
 1970 1975 1980
 Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro
 1985 1990 1995

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

C1
 Cont.

ATT Ile 1	TCT Ser	TGT Cys	GGC Gly	TCT Ser 5	CCT Pro	CCG Pro	CCT Pro	ATC Ile	CTA Leu 10	AAT Asn	GGC Gly	CGG Arg	ATT Ile	AGT Ser 15	TAT Tyr	48
TAT Tyr	TCT Ser	ACC Thr	CCC Pro 20	ATT Ile	GCT Ala	GTT Val	GGT Gly	ACC Thr 25	GTG Val	ATA Ile	AGG Arg	TAC Tyr	AGT Ser 30	TGT Cys	TCA Ser	96
GGT Gly	ACC Thr	TTC Phe 35	CGC Arg	CTC Leu	ATT Ile	GGA Gly	GAA Glu 40	AAA Lys	AGT Ser	CTA Leu	TTA Leu	TGC Cys 45	ATA Ile	ACT Thr	AAA Lys	144
GAC Asp	AAA Lys 50	GTG Val	GAT Asp	GGA Gly	ACC Thr	TGG Trp 55	GAT Asp	AAA Lys	CCT Pro	GCT Ala	CCT Pro 60	AAA Lys	TGT Cys	GAA Glu	TAT Tyr	192
TTC Phe 65	AAT Asn	AAA Lys	TAT Tyr	TCT Ser	TCT Ser 70	TGC Cys	CCT Pro	GAG Glu	CCC Pro	ATA Ile 75	GTA Val	CCA Pro	GGA Gly	GGA Gly	TAC Tyr 80	240
AAA Lys	ATT Ile	AGA Arg	GGC Gly	TCT Ser 85	ACA Thr	CCC Pro	TAC Tyr	AGA Arg	CAT His 90	GGT Gly	GAT Asp	TCT Ser	GTG Val	ACA Thr 95	TTT Phe	288
GCC Ala	TGT Cys	AAA Lys	ACC Thr 100	AAC Asn	TTC Phe	TCC Ser	ATG Met	AAC Asn 105	GGA Gly	AAC Asn	AAG Lys	TCT Ser	GTT Val 110	TGG Trp	TGT Cys	336
CAA Gln	GCA Ala	AAT Asn 115	AAT Asn	ATG Met	TGG Trp	GGG Gly	CCG Pro 120	ACA Thr	CGA Arg	CTA Leu	CCA Pro	ACC Thr 125	TGT Cys	GTA Val	AGT Ser	384
GTT Val 130	TTC Phe	CCT Pro	CTC Leu	GAG Glu	TGT Cys	CCA Pro 135	GCA Ala	CTT Leu	CCT Pro	ATG Met	ATC Ile 140	CAC His	AAT Asn	GGA Gly	CAT His	432
CAC His 145	ACA Thr	AGT Ser	GAG Glu	AAT Asn 150	GTT Val	GGC Gly	TCC Ser	ATT Ile	GCT Ala 155	CCA Pro	GGA Gly	TTG Leu	TCT Ser	GTG Val 160	ACT Thr	480
TAC Tyr	AGC Ser	TGT Cys	GAA Glu	TCT Ser 165	GGT Gly	TAC Tyr	TTG Leu	CTT Leu	GTT Val 170	GGA Gly	GAA Glu	AAG Lys	ATC Ile	ATT Ile 175	AAC Asn	528
TGT Cys	TTG Leu	TCT Ser	TCG Ser 180	GGA Gly	AAA Lys	TGG Trp	AGT Ser	GCT Ala 185	GTC Val	CCC Pro	CCC Pro	ACA Thr	TGT Cys 190	GAA Glu	GAG Glu	576
GCA Ala	CGC Arg	TGT Cys 195	AAA Lys	TCT Ser	CTA Leu	GGA Gly	CGA Arg 200	TTT Phe	CCC Pro	AAT Asn	GGG Gly	AAG Lys 205	GTA Val	AAG Lys	GAG Glu	624
CCT Pro 210	CCA Pro	ATT Ile	CTC Leu	CGG Arg	GTT Val	GGT Gly	GTA Val 215	ACT Thr	GCA Ala	AAC Asn	TTT Phe 220	TTC Phe	TGT Cys	GAT Asp	GAA Glu	672
GGG Gly 225	TAT Tyr	CGA Arg	CTG Leu	CAA Gln	GGC Gly 230	CCA Pro	CCT Pro	TCT Ser	AGT Ser	CGG Arg 235	TGT Cys	GTA Val	ATT Ile	GCT Ala	GGA Gly 240	720

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Cont.

CAG GGA GTT GCT TGG ACC AAA ATG CCA GTA TGT GAA GAA ATT TTT TGC Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu Glu Ile Phe Cys 245 250 255	768
CCA TCA CCT CCC CCT ATT CTC AAT GGA AGA CAT ATA GGC AAC TCA CTA Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile Gly Asn Ser Leu 260 265 270	816
GCA AAT GTC TCA TAT GGA AGC ATA GTC ACT TAC ACT TGT GAC CCG GAC Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr Cys Asp Pro Asp 275 280 285	864
CCA GAG GAA GGA GTG AAC TTC ATC CTT ATT GGA GAG AGC ACT CTC CGT Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu Ser Thr Leu Arg 290 295 300	912
TGT ACA GTT GAT AGT CAG AAG ACT GGG ACC TGG AGT GGC CCT GCC CCA Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser Gly Pro Ala Pro 305 310 315 320	960
CGC TGT GAA CTT TCT ACT TCT GCG GTT CAG TGT CCA CAT CCC CAG ATC Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro His Pro Gln Ile 325 330 335	1008
CTA AGA GGC CGA ATG GTA TCT GGG CAG AAA GAT CGA TAT ACC TAT AAC Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg Tyr Thr Tyr Asn 340 345 350	1056
GAC ACT GTG ATA TTT GCT TGC ATG TTT GGC TTC ACC TTG AAG GGC AGC Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr Leu Lys Gly Ser 355 360 365	1104
AAG CAA ATC CGA TGC AAT GCC CAA GGC ACA TGG GAG CCA TCT GCA CCA Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu Pro Ser Ala Pro 370 375 380	1152
GTC TGT GAA AAG GAA TGC CAG GCC CCT CCT AAC ATC CTC AAT GGG CAA Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile Leu Asn Gly Gln 385 390 395 400	1200
AAG GAA GAT AGA CAC ATG GTC CGC TTT GAC CCT GGA ACA TCT ATA AAA Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly Thr Ser Ile Lys 405 410 415	1248
TAT AGC TGT AAC CCT GGC TAT GTG CTG GTG GGA GAA GAA TCC ATA CAG Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu Glu Ser Ile Gln 420 425 430	1296
TGT ACC TCT GAG GTG TGG ACA CCC CCT GTA CCC CAA TGC AAA GTG GCA Cys Thr Ser Glu Val Trp Thr Pro Pro Val Pro Gln Cys Lys Val Ala 435 440 445	1344
GCG TGT GAA GCT ACA GGA AGG CAA CTC TTG ACA AAA CCC CAG CAC CAA Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr Lys Pro Gln His Gln 450 455 460	1392
TTT GTT AGA CCA GAT GTC AAC TCT TCT TGT GGT GAA GGG TAC AAG TTA Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly Glu Gly Tyr Lys Leu 465 470 475 480	1440

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Cont.

AGT	GGG	AGT	GTT	TAT	CAG	GAG	TGT	CAA	GGC	ACA	ATT	CCT	TGG	TTT	ATG	1488
Ser	Gly	Ser	Val	Tyr	Gln	Glu	Cys	Gln	Gly	Thr	Ile	Pro	Trp	Phe	Met	
				485					490					495		
GAG	ATT	CGT	CTT	TGT	AAA	GAA	ATC	ACC	TGC	CCA	CCA	CCC	CCT	GTT	ATC	1536
Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro	Pro	Pro	Pro	Val	Ile	
			500					505					510			
TAC	AAT	GGG	GCA	CAC	ACC	GGG	AGT	TCC	TTA	GAA	GAT	TTT	CCA	TAT	GGA	1584
Tyr	Asn	Gly	Ala	His	Thr	Gly	Ser	Ser	Leu	Glu	Asp	Phe	Pro	Tyr	Gly	
		515					520					525				
ACC	ACG	GTC	ACT	TAC	ACA	TGT	AAC	CCT	GGG	CCA	GAA	AGA	GGA	GTG	GAA	1632
Thr	Thr	Val	Thr	Tyr	Thr	Cys	Asn	Pro	Gly	Pro	Glu	Arg	Gly	Val	Glu	
		530				535					540					
TTC	AGC	CTC	ATT	GGA	GAG	AGC	ACC	ATC	CGT	TGT	ACA	AGC	AAT	GAT	CAA	1680
Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asn	Asp	Gln	
545					550				555						560	
GAA	AGA	GGC	ACC	TGG	AGT	GGC	CCT	GCT	CCC	CTG	TGT	AAA	CTT	TCC	CTC	1728
Glu	Arg	Gly	Thr	Trp	Ser	Gly	Pro	Ala	Pro	Leu	Cys	Lys	Leu	Ser	Leu	
				565					570					575		
CTT	GCT	GTC	CAG	TGC	TCA	CAT	GTC	CAT	ATT	GCA	AAT	GGA	TAC	AAG	ATA	1776
Leu	Ala	Val	Gln	Cys	Ser	His	Val	His	Ile	Ala	Asn	Gly	Tyr	Lys	Ile	
			580					585					590			
TCT	GGC	AAG	GAA	GCC	CCA	TAT	TTC	TAC	AAT	GAC	ACT	GTG	ACA	TTC	AAG	1824
Ser	Gly	Lys	Glu	Ala	Pro	Tyr	Phe	Tyr	Asn	Asp	Thr	Val	Thr	Phe	Lys	
		595					600					605				
TGT	TAT	AGT	GGA	TTT	ACT	TTG	AAG	GGC	AGT	AGT	CAG	ATT	CGT	TGC	AAA	1872
Cys	Tyr	Ser	Gly	Phe	Thr	Leu	Lys	Gly	Ser	Ser	Gln	Ile	Arg	Cys	Lys	
		610					615				620					
GCT	GAT	AAC	ACC	TGG	GAT	CCT	GAA	ATA	CCA	GTT	TGT	GAA	AAA	GAA	ACA	1920
Ala	Asp	Asn	Thr	Trp	Asp	Pro	Glu	Ile	Pro	Val	Cys	Glu	Lys	Glu	Thr	
625					630					635				640		
TGC	CAG	CAT	GTG	AGA	CAG	AGT	CTT	CAA	GAA	CTT	CCA	GCT	GGT	TCA	CGT	1968
Cys	Gln	His	Val	Arg	Gln	Ser	Leu	Gln	Glu	Leu	Pro	Ala	Gly	Ser	Arg	
				645					650					655		
GTG	GAG	CTA	GTT	AAT	ACG	TCC	TGC	CAA	GAT	GGG	TAC	CAG	TTG	ACT	GGA	2016
Val	Glu	Leu	Val	Asn	Thr	Ser	Cys	Gln	Asp	Gly	Tyr	Gln	Leu	Thr	Gly	
			660					665					670			
CAT	GCT	TAT	CAG	ATG	TGT	CAA	GAT	GCT	GAA	AAT	GGA	ATT	TGG	TTC	AAA	2064
His	Ala	Tyr	Gln	Met	Cys	Gln	Asp	Ala	Glu	Asn	Gly	Ile	Trp	Phe	Lys	
			675				680					685				
AAG	ATT	CCA	CTT	TGT	AAA	GTT	ATT	CAC	TGT	CAC	CCT	CCA	CCA	GTG	ATT	2112
Lys	Ile	Pro	Leu	Cys	Lys	Val	Ile	His	Cys	His	Pro	Pro	Pro	Val	Ile	
		690					695				700					
GTC	AAT	GGG	AAG	CAC	ACA	GGC	ATG	ATG	GCA	GAA	AAC	TTT	CTA	TAT	GGA	2160
Val	Asn	Gly	Lys	His	Thr	Gly	Met	Met	Ala	Glu	Asn	Phe	Leu	Tyr	Gly	
705					710					715					720	

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Cont.

AAT	GAA	GTC	TCT	TAT	GAA	TGT	GAC	CAA	GGA	TTC	TAT	CTC	CTG	GGA	GAG	2208
Asn	Glu	Val	Ser	Tyr	Glu	Cys	Asp	Gln	Gly	Phe	Tyr	Leu	Leu	Gly	Glu	
				725					730					735		
AAA	AAA	TTG	CAG	TGC	AGA	AGT	GAT	TCT	AAA	GGA	CAT	GGA	TCT	TGG	AGC	2256
Lys	Lys	Leu	Gln	Cys	Arg	Ser	Asp	Ser	Lys	Gly	His	Gly	Ser	Trp	Ser	
			740					745					750			
GGG	CCT	TCC	CCA	CAG	TGC	TTA	CGA	TCT	CCT	CCT	GTG	ACT	CGC	TGC	CCT	2304
Gly	Pro	Ser	Pro	Gln	Cys	Leu	Arg	Ser	Pro	Pro	Val	Thr	Arg	Cys	Pro	
		755					760					765				
AAT	CCA	GAA	GTC	AAA	CAT	GGG	TAC	AAG	CTC	AAT	AAA	ACA	CAT	TCT	GCA	2352
Asn	Pro	Glu	Val	Lys	His	Gly	Tyr	Lys	Leu	Asn	Lys	Thr	His	Ser	Ala	
	770					775					780					
TAT	TCC	CAC	AAT	GAC	ATA	GTG	TAT	GTT	GAC	TGC	AAT	CCT	GGC	TTC	ATC	2400
Tyr	Ser	His	Asn	Asp	Ile	Val	Tyr	Val	Asp	Cys	Asn	Pro	Gly	Phe	Ile	
785					790					795					800	
ATG	AAT	GGT	AGT	CGC	GTG	ATT	AGG	TGT	CAT	ACT	GAT	AAC	ACA	TGG	GTG	2448
Met	Asn	Gly	Ser	Arg	Val	Ile	Arg	Cys	His	Thr	Asp	Asn	Thr	Trp	Val	
				805					810					815		
CCA	GGT	GTG	CCA	ACT	TGT	ATC	AAA	AAA	GCC	TTC	ATA	GGG	TGT	CCA	CCT	2496
Pro	Gly	Val	Pro	Thr	Cys	Ile	Lys	Lys	Ala	Phe	Ile	Gly	Cys	Pro	Pro	
			820					825					830			
CCG	CCT	AAG	ACC	CCT	AAC	GGG	AAC	CAT	ACT	GGT	GGA	AAC	ATA	GCT	CGA	2544
Pro	Pro	Lys	Thr	Pro	Asn	Gly	Asn	His	Thr	Gly	Gly	Asn	Ile	Ala	Arg	
		835					840					845				
TTT	TCT	CCT	GGA	ATG	TCA	ATC	CTG	TAC	AGC	TGT	GAC	CAA	GGC	TAC	CTG	2592
Phe	Ser	Pro	Gly	Met	Ser	Ile	Leu	Tyr	Ser	Cys	Asp	Gln	Gly	Tyr	Leu	
850						855					860					
CTG	GTG	GGA	GAG	GCA	CTC	CTT	CTT	TGC	ACA	CAT	GAG	GGA	ACC	TGG	AGC	2640
Leu	Val	Gly	Glu	Ala	Leu	Leu	Leu	Cys	Thr	His	Glu	Gly	Thr	Trp	Ser	
865					870					875					880	
CAA	CCT	GCC	CCT	CAT	TGT	AAA	GAG	GTA	AAC	TGT	AGC	TCA	CCA	GCA	GAT	2688
Gln	Pro	Ala	Pro	His	Cys	Lys	Glu	Val	Asn	Cys	Ser	Ser	Pro	Ala	Asp	
				885					890					895		
ATG	GAT	GGA	ATC	CAG	AAA	GGG	CTG	GAA	CCA	AGG	AAA	ATG	TAT	CAG	TAT	2736
Met	Asp	Gly	Ile	Gln	Lys	Gly	Leu	Glu	Pro	Arg	Lys	Met	Tyr	Gln	Tyr	
			900					905					910			
GGA	GCT	GTT	GTA	ACT	CTG	GAG	TGT	GAA	GAT	GGG	TAT	ATG	CTG	GAA	GGC	2784
Gly	Ala	Val	Val	Thr	Leu	Glu	Cys	Glu	Asp	Gly	Tyr	Met	Leu	Glu	Gly	
		915					920					925				
AGT	CCC	CAG	AGC	CAG	TGC	CAA	TCG	GAT	CAC	CAA	TGG	AAC	CCT	CCC	CTG	2832
Ser	Pro	Gln	Ser	Gln	Cys	Gln	Ser	Asp	His	Gln	Trp	Asn	Pro	Pro	Leu	
	930					935					940					
GCG	GTT	TGC	AGA	TCC	CGT	TCA	CTT	GCT	CCT	GTC	CTT	TGT	GGT	ATT	GCT	2880
Ala	Val	Cys	Arg	Ser	Arg	Ser	Leu	Ala	Pro	Val	Leu	Cys	Gly	Ile	Ala	
945					950					955					960	

Cont.

GCA GGT TTG ATA CTT CTT ACC TTC TTG ATT GTC GTT ACC TTA TAC GTG	2928
Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val Val Thr Leu Tyr Val	
965 970 975	
ATA TCA AAA CAC AGA GCA CGC AAT TAT TAT ACA GAT ACA AGC CAG AAA	2976
Ile Ser Lys His Arg Ala Arg Asn Tyr Tyr Thr Asp Thr Ser Gln Lys	
980 985 990	
GAA GCT TTT CAT TTA GAA GCA CGA GAA GTA TAT TCT GTT GAT CCA TAC	3024
Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr Ser Val Asp Pro Tyr	
995 1000 1005	
AAC CCA GCC AGC	3036
Asn Pro Ala Ser	
1010	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1 5 10 15
 Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
 20 25 30
 Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
 35 40 45
 Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
 50 55 60
 Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
 65 70 75 80
 Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
 85 90 95
 Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
 100 105 110
 Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
 115 120 125
 Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
 130 135 140
 His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
 145 150 155 160
 Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
 165 170 175

C1
Cont

Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
 180 185 190
 Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
 195 200 205
 Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
 210 215 220
 Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
 225 230 235 240
 Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu Glu Ile Phe Cys
 245 250 255
 Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile Gly Asn Ser Leu
 260 265 270
 Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr Cys Asp Pro Asp
 275 280 285
 Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu Ser Thr Leu Arg
 290 295 300
 Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser Gly Pro Ala Pro
 305 310 315 320
 Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro His Pro Gln Ile
 325 330 335
 Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg Tyr Thr Tyr Asn
 340 345 350
 Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr Leu Lys Gly Ser
 355 360 365
 Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu Pro Ser Ala Pro
 370 375 380
 Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile Leu Asn Gly Gln
 385 390 395 400
 Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly Thr Ser Ile Lys
 405 410 415
 Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu Glu Ser Ile Gln
 420 425 430
 Cys Thr Ser Glu Val Trp Thr Pro Pro Val Pro Gln Cys Lys Val Ala
 435 440 445
 Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr Lys Pro Gln His Gln
 450 455 460
 Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly Glu Gly Tyr Lys Leu
 465 470 475 480
 Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr Ile Pro Trp Phe Met
 485 490 495
 Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro Pro Pro Pro Val Ile
 500 505 510

C¹
 Cont.

Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu Asp Phe Pro Tyr Gly
 515 520 525
 Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro Glu Arg Gly Val Glu
 530 535 540
 Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asn Asp Gln
 545 550 555 560
 Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu Cys Lys Leu Ser Leu
 565 570 575
 Leu Ala Val Gln Cys Ser His Val His Ile Ala Asn Gly Tyr Lys Ile
 580 585 590
 Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp Thr Val Thr Phe Lys
 595 600 605
 Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser Gln Ile Arg Cys Lys
 610 615 620
 Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val Cys Glu Lys Glu Thr
 625 630 635 640
 Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu Pro Ala Gly Ser Arg
 645 650 655
 Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly Tyr Gln Leu Thr Gly
 660 665 670
 His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn Gly Ile Trp Phe Lys
 675 680 685
 Lys Ile Pro Leu Cys Lys Val Ile His Cys His Pro Pro Pro Val Ile
 690 695 700
 Val Asn Gly Lys His Thr Gly Met Met Ala Glu Asn Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro Val Thr Arg Cys Pro
 755 760 765
 Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys Asn Pro Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser Arg Val Ile Arg Cys His Thr Asp Asn Thr Trp Val
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Lys Lys Ala Phe Ile Gly Cys Pro Pro
 820 825 830
 Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly Gly Asn Ile Ala Arg
 835 840 845

C¹
 Cont.

Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys Asp Gln Gly Tyr Leu
 850 855 860
 Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys Ser Ser Pro Ala Asp
 885 890 895
 Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg Lys Met Tyr Gln Tyr
 900 905 910
 Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly Tyr Met Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val Leu Cys Gly Ile Ala
 945 950 955 960
 Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val Val Thr Leu Tyr Val
 965 970 975
 Ile Ser Lys His Arg Ala Arg Asn Tyr Tyr Thr Asp Thr Ser Gln Lys
 980 985 990
 Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr Ser Val Asp Pro Tyr
 995 1000 1005
 Asn Pro Ala Ser
 1010

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA 48
 Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1 5 10 15
 GGC CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA 96
 Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
 20 25 30
 GAA AGC TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ACC TGC CTT 144
 Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Thr Cys Leu
 35 40 45

c1
 Cont

AAG Lys	GGC Gly	ATG Met	CAA Gln	TGG Trp	TCA Ser	GAT Asp	ATT Ile	GAA Glu	GAG Glu	TTC Phe	TGC Cys	AAT Asn	CGT Arg	AGC Ser	TGC Cys	192
	50					55					60					
GAG Glu	GTG Val	CCA Pro	ACA Thr	AGG Arg	CTA Leu	AAT Asn	TCT Ser	GCA Ala	TCC Ser	CTC Leu	AAA Lys	CAG Gln	CCT Pro	TAT Tyr	ATC Ile	240
65					70					75					80	
ACT Thr	CAG Gln	AAT Asn	TAT Tyr	TTT Phe	CCA Pro	GTC Val	GGT Gly	ACT Thr	GTT Val	GTG Val	GAA Glu	TAT Tyr	GAG Glu	TGC Cys	CGT Arg	288
				85					90					95		
CCA Pro	GGT Gly	TAC Tyr	AGA Arg	AGA Arg	GAA Glu	CCT Pro	TCT Ser	CTA Leu	TCA Ser	CCA Pro	AAA Lys	CTA Leu	ACT Thr	TGC Cys	CTT Leu	336
			100					105					110			
CAG Gln	AAT Asn	TTA Leu	AAA Lys	TGG Trp	TCC Ser	ACA Thr	GCA Ala	GTC Val	GAA Glu	TTT Phe	TGT Cys	AAA Lys	AAG Lys	AAA Lys	TCA Ser	384
		115				120						125				
TGC Cys	CCT Pro	AAT Asn	CCG Pro	GGA Gly	GAA Glu	ATA Ile	CGA Arg	AAT Asn	GGT Gly	CAG Gln	ATT Ile	GAT Asp	GTA Val	CCA Pro	GGT Gly	432
130						135					140					
GGC Gly	ATA Ile	TTA Leu	TTT Phe	GGT Gly	GCA Ala	ACC Thr	ATC Ile	TCC Ser	TTC Phe	TCA Ser	TGT Cys	AAC Asn	ACA Thr	GGG Gly	TAC Tyr	480
145					150					155					160	
AAA Lys	TTA Leu	TTT Phe	GGC Gly	TCG Ser	ACT Thr	TCT Ser	AGT Ser	TTT Phe	TGT Cys	CTT Leu	ATT Ile	TCA Ser	GGC Gly	AGC Ser	TCT Ser	528
				165					170					175		
GTC Val	CAG Gln	TGG Trp	AGT Ser	GAC Asp	CCG Pro	TTG Leu	CCA Pro	GAG Glu	TGC Cys	AGA Arg	GAA Glu	ATT Ile	TAT Tyr	TGT Cys	CCA Pro	576
			180					185					190			
GCA Ala	CCA Pro	CCA Pro	CAA Gln	ATT Ile	GAC Asp	AAT Asn	GGA Gly	ATA Ile	ATT Ile	CAA Gln	GGG Gly	GAA Glu	CGT Arg	GAC Asp	CAT His	624
		195					200					205				
TAT Tyr	GGA Gly	TAT Tyr	AGA Arg	CAG Gln	TCT Ser	GTA Val	ACG Thr	TAT Tyr	GCA Ala	TGT Cys	AAT Asn	AAA Lys	GGA Gly	TTC Phe	ACC Thr	672
	210					215					220					
ATG Met	ATT Ile	GGA Gly	GAG Glu	CAC His	TCT Ser	ATT Ile	TAT Tyr	TGT Cys	ACT Thr	GTG Val	AAT Asn	AAT Asn	GAT Asp	GAA Glu	GGA Gly	720
225					230					235					240	
GAG Glu	TGG Trp	AGT Ser	GGC Gly	CCA Pro	CCA Pro	CCT Pro	GAA Glu	TGC Cys	AGA Arg	GGA Gly	AAA Lys	TCT Ser	CTA Leu	ACT Thr	TCC Ser	768
				245					250					255		
AAG Lys	GTC Val	CCA Pro	CCA Pro	ACA Thr	GTT Val	CAG Gln	AAA Lys	CCT Pro	ACC Thr	ACA Thr	GTA Val	AAT Asn	GTT Val	CCA Pro	ACT Thr	816
			260				265						270			
ACA Thr	GAA Glu	GTC Val	TCA Ser	CCA Pro	ACT Thr	TCT Ser	CAG Gln	AAA Lys	ACC Thr	ACC Thr	ACA Thr	AAA Lys	ACC Thr	ACC Thr	ACA Thr	864
		275					280					285				

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Cont.

CCA AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG 912
 Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys
 290 295 300

CAT TTT CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT 960
 His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly
 305 310 315 320

ACT ACC CGT CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG 1008
 Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu
 325 330 335

CTT GGG ACG CTA GTA ACC ATG GGC TTG CTG ACT TAGCCAAAGA AGAGTTAAGA 1061
 Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
 340 345

AGAAAATACA CACAAGTATA CAGACTGTTC CTAGTTTCTT AGACTTATCT GCATATTGGA 1121

TAAAATAAAT GCAATTGTGC TCTTCATTTA GGATGCTTTC ATTGTCTTTA AGATGTGTTA 1181

GGAATGTCAA CAGAGCAAGG AGAAAAAAGG CAGTCCCTGGA ATCACATTCT TAGCACACCT 1241

GCGCCTCTTG AAAATAGAAC AACTTGCAGA ATTGAGAGTG ATTCCCTTTCC TAAAAGTGTA 1301

AGAAAGCATA GAGATTTGTT CGTATTAAGA ATGGGATCAC GAGGAAAAGA GAAGGAAAGT 1361

GATTTTTTTTC CACAAGATCT GAAATGATAT TTCCACTTAT AAAGGAAATA AAAAATGAAA 1421

AACATTATTTT GGATATCAAA AGCAAATAAA AACCCTTTC AGTCTCTTCT AAGCAAAATT 1481

GCTAAAGAGA GATGACCACA TTATAAAGTA ATCTTTGGCT AAGGCATTTT CATCTTTCTT 1541

TCGGTTGGCA AAATATTTTA AAGGTAAAAC ATGCTGGTGA ACCAGGGTGT TGATGGTGAT 1601

AAGGGAGGAA TATAGAATGA AAGACTGAAT CTTCCCTTTGT TGCACAAATA GAGTTTGGAA 1661

AAAGCCTGTG AAAGGTGTCT TCTTTGACTT AATGTCTTTA AAAGTATCCA GAGATACTAC 1721

AATATTAACA TAAGAAAAGA TTATATATTA TTTCTGAATC GAGATGTCCA TAGTCAAATT 1781

TGTAAATCTT ATTCTTTTGT AATATTTTAT TATATTTAT TATGACAGTG AACATTTCTGA 1841

TTTTACATGT AAAACAAGAA AAGTTGAAGA AGATATGTGA AGAAAAATGT ATTTTTCCTA 1901

AATAGAAATA AATGATCCCA TTTTTTGGT 1930

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1 5 10 15

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cont

Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
 20 25 30
 Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Thr Cys Leu
 35 40 45
 Lys Gly Met Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
 50 55 60
 Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
 65 70 75 80
 Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
 85 90 95
 Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
 100 105 110
 Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser
 115 120 125
 Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
 130 135 140
 Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
 145 150 155 160
 Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
 165 170 175
 Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
 180 185 190
 Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
 195 200 205
 Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
 210 215 220
 Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
 225 230 235 240
 Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser
 245 250 255
 Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr
 260 265 270
 Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr
 275 280 285
 Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys
 290 295 300
 His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly
 305 310 315 320
 Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu
 325 330 335
 Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
 340 345

C!
 cont.

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGT GAG GAG CCA CCA ACA TTT GAA GCT ATG GAG CTC ATT GGT AAA CCA 48
 Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro
 1 5 10 15

AAA CCC TAC TAT GAG ATT GGT GAA CGA GTA GAT TAT AAG TGT AAA AAA 96
 Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys
 20 25 30

GGA TAC TTC TAT ATA CCT CCT CTT GCC ACC CAT ACT ATT TGT GAT CGG 144
 Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg
 35 40 45

AAT CAT ACA TGG CTA CCT GTC TCA GAT GAC GCC TGT TAT AGA GAA ACA 192
 Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr
 50 55 60

TGT CCA TAT ATA CGG GAT CCT TTA AAT GGC CAA GCA GTC CCT GCA AAT 240
 Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro Ala Asn
 65 70 75 80

GGG ACT TAC GAG TTT GGT TAT CAG ATG CAC TTT ATT TGT AAT GAG GGT 288
 Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly
 85 90 95

TAT TAC TTA ATT GGT GAA GAA ATT CTA TAT TGT GAA CTT AAA GGA TCA 336
 Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser
 100 105 110

GTA GCA ATT TGG AGC GGT AAG CCC CCA ATA TGT GAA AAG GTT TTG TGT 384
 Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys
 115 120 125

ACA CCA CCT CCA AAA ATA AAA AAT GGA AAA CAC ACC TTT AGT GAA GTA 432
 Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val
 130 135 140

GAA GTA TTT GAG TAT CTT GAT GCA GTA ACT TAT AGT TGT GAT CCT GCA 480
 Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp Pro Ala
 145 150 155 160

CCT GGA CCA GAT CCA TTT TCA CTT ATT GGA GAG AGC ACG ATT TAT TGT 528
 Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys
 165 170 175

C1
 cont.

GGT GAC AAT TCA GTG TGG AGT CGT GCT GCT CCA GAG TGT AAA GTG GTC 576
 Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val
 180 185 190

AAA TGT CGA TTT CCA GTA GTC GAA AAT GGA AAA CAG ATA TCA GGA TTT 624
 Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe
 195 200 205

GGA AAA AAA TTT TAC TAC AAA GCA ACA GTT ATG TTT GAA TGC GAT AAG 672
 Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys
 210 215 220

GGT TTT TAC CTC GAT GGC AGC GAC ACA ATT GTC TGT GAC AGT AAC AGT 720
 Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser
 225 230 235 240

ACT TGG GAT CCC CCA GTT CCA AAG TGT CTT AAA GTG TCG ACT TCT TCC 768
 Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr Ser Ser
 245 250 255

ACT ACA AAA TCT CCA GCG TCC AGT GCC TCA GGT CCT AGG CCT ACT TAC 816
 Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro Thr Tyr
 260 265 270

AAG CCT CCA GTC TCA AAT TAT CCA GGA TAT CCT AAA CCT GAG GAA GGA 864
 Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu Glu Gly
 275 280 285

ATA CTT GAC AGT TTG GAT GTT TGG GTC ATT GCT GTG ATT GTT ATT GCC 912
 Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val Ile Ala
 290 295 300

ATA GTT GTT GGA GTT GCA GTA ATT TGT GTT GTC CCG TAC AGA TAT CTT 960
 Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg Tyr Leu
 305 310 315 320

CAA AGG AGG AAG AAG AAA GGG AAA GCA GAT GGT GGA GCT GAA TAT GCC 1008
 Gln Arg Arg Lys Lys Lys Gly Lys Ala Asp Gly Gly Ala Glu Tyr Ala
 325 330 335

ACT TAC CAG ACT AAA TCA ACC ACT CCA GCA GAG CAG AGA GGC 1050
 Thr Tyr Gln Thr Lys Ser Thr Thr Pro Ala Glu Gln Arg Gly
 340 345 350

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro
 1 5 10 15

Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys
 20 25 30

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cont

Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg
 35 40 45
 Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr
 50 55 60
 Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro Ala Asn
 65 70 75 80
 Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly
 85 90 95
 Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser
 100 105 110
 Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys
 115 120 125
 Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val
 130 135 140
 Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp Pro Ala
 145 150 155 160
 Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys
 165 170 175
 Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val
 180 185 190
 Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe
 195 200 205
 Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys
 210 215 220
 Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser
 225 230 235 240
 Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr Ser Ser
 245 250 255
 Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro Thr Tyr
 260 265 270
 Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu Glu Gly
 275 280 285
 Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val Ile Ala
 290 295 300
 Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg Tyr Leu
 305 310 315 320
 Gln Arg Arg Lys Lys Lys Gly Lys Ala Asp Gly Gly Ala Glu Tyr Ala
 325 330 335
 Thr Tyr Gln Thr Lys Ser Thr Thr Pro Ala Glu Gln Arg Gly
 340 345 350

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 Cont